

IN THE CLAIMS

1. (Original) A method for identifying candidate genes capable of producing hybrid vigour in an animal or plant, comprising the steps of:

- (i) comparing the nucleotide sequence of alleles of candidate genes isolated from an animal or plant which exhibits hybrid vigour with the nucleotide sequences from the corresponding alleles isolated from the parents of said animal or plant;
- (ii) identifying nucleotide sequence differences in the alleles from said animal or plant which exhibits hybrid vigour which codes for amino acid sequence variation; and
- (iii) identifying that the amino acid sequence variation between alleles of the candidate gene in said animal or plant is encoded by nucleotide sequences which are located within two or more different exons within the candidate gene.

2.(Currently amended) The [[A]] method according to claim 1, wherein the amino acid sequence variation is a conservative modified variation.

3. (Currently amended) The [[A]] method according to claim 1, wherein the amino acid sequence variation is a non-conservative modified variation.

4. (Currently amended) The [[A]] method according to claim 1, wherein the step of identifying the nucleotide sequence difference comprises the step of sequencing the nucleotide sequence isolated from said ~~plant or animal~~ or plant.

5. (Currently amended) The [[A]] method according to claim 1, wherein the plant is selected from the group consisting of barley, rye, sorghum, maize, soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane, banana, blackberry, blueberry, strawberry, [[and]] raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, ~~grapes~~ grape, honeydew, lettuce, mango, melon, onion, papaya, [[peas]] pea, ~~peppers~~ pepper, pineapple, spinach, squash, sweet corn, tobacco,

tomato, watermelon, rosaceous fruits (~~such as~~ including apple, peach, pear, cherry, and plum), ~~[[and]]~~ vegetable brassicas (~~such as~~ including broccoli, cabbage, cauliflower, brussel sprouts, and kohlrabi). ~~Other crops, fruits and vegetables whose phenotype may be changed include barley, currant, avocado, citrus fruits such as~~ (including oranges, lemons, grapefruit, and tangerines), artichoke, cherries, nuts ~~such as the~~ (including walnut and peanut), endive, leek, roots ~~, such as~~ (including arrowroot, beet, cassava, turnip, radish, yam, sweet potato), and ~~[[beans]]~~ bean.

6.(Currently amended) The ~~[[A]]~~ method according to claim 1, wherein the animal is selected from the group consisting of a mammal ~~[[or]]~~ and a fish.

7.(Currently amended) The ~~[[A]]~~ method according to claim 6, wherein the mammal is selected from the group consisting of the mammalian Orders Primates, Rodentia, Lagomorpha, Cetacea, Carnivora, Perissodactyla, and Artiodactyla.

8.(Currently amended) The ~~[[A]]~~ method according to claim 7, wherein the Artiodactyla is selected from the group consisting ~~[[one]]~~ of the ~~[[nine]]~~ families ~~[[,]]~~ Suidae, Tayassuidae, Hippopotamidae, Camelidae, Tragulidae, Giraffidae, Cervidae, Antilocapridae, and Bovidae.

9. (Currently amended) The ~~[[A]]~~ method according to claim 8, wherein the animal selected from Bovidae is an ungulate.

10. (Currently amended) The ~~[[A]]~~ method according to claim 9, wherein the ungulate is selected from the group consisting of cows, ~~[[or]]~~ bulls, bison, buffalo, sheep, big-horn sheep, horses, ponies, donkeys, mule, deer, elk, caribou, goat, water buffalo, camels, llama, alpaca, and pigs.

11. (Currently amended) The ~~[[A]]~~ method according to claim 6, wherein the animal is a fish.

12. (Currently amended) The [[A]] method according to claim 11, wherein the fish is selected from the group consisting of zebrafish, European carp, salmon, mosquito fish, tench, lampreys, round gobies, tilapia, and trout.

13. (Currently amended) The [[A]] method according to claim 8 7, wherein the [[animal]] mammal is a human.

14. (Original) A method for identifying candidate genes capable of producing hybrid debility (HD) in an animal or plant, comprising the steps of:

- (i) comparing the nucleotide sequence of alleles of candidate genes isolated from an animal or plant which exhibits said hybrid debility (HD) with the nucleotide sequences from the corresponding alleles isolated from the parents of said animal or plant;
- (ii) identifying nucleotide sequence differences in the alleles from said animal or plant which exhibits said hybrid debility (HD) which codes for amino acid sequence variation; and
- (iii) identifying that the amino acid sequence variation between alleles of the candidate gene in said animal or plant is encoded by nucleotide sequences which are located within two or more different exons within the candidate gene.

15. (Currently amended) The [[A]] method according to claim 14, wherein the amino acid sequence variation is a conservative modified variation.

16. (Currently amended) The [[A]] method according to claim 14, wherein the amino acid sequence variation is a non-conservative modified variation.

17. (Currently amended) The [[A]] method according to claim 14, wherein the step of identifying the nucleotide sequence difference comprises the step of sequencing the nucleotide sequence isolated from said ~~plant or animal~~ or plant.

18. (Currently amended) The [[A]] method according to claim 14, wherein the plant is

selected from the group consisting of a weed ~~[[or]]~~ and other noxious plant.

19. (Currently amended) The ~~[[A]]~~ method according to claim 14, wherein the animal is a pest.

20. (Currently amended) The ~~[[A]]~~ method according to claim 19, wherein the pest animal is selected from the group consisting of a rodent, a rabbit, ~~[[or]]~~ and a fish.

21. (Currently amended) A method for producing hybrid vigour or hybrid debility in an animal or plant, comprising the steps of:

- (i) comparing the nucleotide sequence of alleles isolated from a gene from an animal or plant which promotes hybrid vigour or hybrid debility with the nucleotide sequences from the corresponding alleles isolated from the parents of said animal or plant;
- (ii) identifying nucleotide sequence differences in the alleles from said animal or plant which promote hybrid vigour or hybrid debility which code for amino acid sequence variation; ~~[[and]]~~
- (iii) identifying that the amino acid sequence variation between alleles of the candidate gene in said animal or plant is encoded by nucleotide sequences which are located within two or more different exons within the candidate gene ~~[[.]]~~ ;
- (iv) preparing a construct comprising nucleotide sequence from the alleles which promotes hybrid vigour or hybrid debility within said animal or plant;
- (v) transforming said construct into a recipient ~~plant or animal~~ or plant cell; and
- (vi) regenerating ~~a plant or~~ the animal or plant, which expresses said construct, from said cell.

22. (Currently amended) A method ~~[[of]]~~ for detecting the presence or absence of hybrid mRNA in a plant or animal comprising the steps of :

- (i) isolating mRNA from a plant or animal;
- (ii) comparing the nucleotide sequence of said mRNA to the

corresponding coding sequences of the plant's or animal's alleles; and

(iii) determining whether or not the mRNA sequence comprises nucleotide sequences from two or more different exons.

23. (Currently amended) A construct comprising a synthetic gene, the synthetic gene comprising exons from different alleles of a gene, wherein said exons code for amino acid sequence variation found in only one allele, such that said synthetic gene does not contain a nucleotide sequence that is the same as either allele and is capable of producing hybrid mRNA.

24. (Currently amended) A method for using the ~~Use of hybrid mRNA molecules produced by a construct~~ according to claim 23 to overcome hybrid debility in a plant or animal and/or induce hybrid vigour in a plant or animal comprising the step of introducing said construct ~~hybrid mRNA~~ into said plant or animal ~~or plant~~.

25. (Currently amended) The method ~~[[Use]]~~ according to claim 24, wherein the step of introducing said construct ~~hybrid mRNA~~ into said plant or animal ~~or plant~~ is by transformation.

26. (Currently amended) The method ~~[[Use]]~~ according to claim 25, wherein the step of transformation into ~~[[a]]~~ the plant is selected from the group consisting of homologous recombination, microprojectile bombardment, PEG mediated transformation, electroporation, silicon carbide fibre mediated transformation, or Agrobacterium-mediated transformation.

27. (Original) A method for producing genetically engineered or transgenic non-human animal by inserting a synthetic gene into a non-human somatic cell or cell nucleus prior to transferring the somatic cell or cell nucleus, wherein said synthetic gene comprises exons from different alleles of a gene, wherein said alleles code for amino acid sequence variation, wherein the variation does not occur in the same allele.

28.(Currently amended) A genetically engineered or transgenic non-human animal obtained by the [[a]] method according to claim 27.

29. (Currently amended) The [[A]] method according to claim 27, wherein the ~~animal~~ cells are isolated from an animal selected from the group consisting of a mammal and a fish.